

QY 482 TGAATGAGCGCTCAGGCTGGGTTGGTTAATGAAATCAGTTGGGTGCGCAGTTCTTG 423
 Db 121 ProSerArgGln-----SerArgLeu 128
 QY 422 GNAAGTCAAAATCTCCGGGTGACTCCACCTCCGGGGCGTGTGGA----- 371
 Db 129 GlnArgHisGlyLeuSerArgCysProLeu-ProLeuArgArgProSerProAla 148
 QY 370 -----TCACATCC 363
 Db 148 aTrpArgGlnProProlleGluLeuGlyAlaValArgLeuArgProProGlnArgArgP 168
 QY 362 TGTTCAGCCCATCTCTTCAGCGCTCTCTCAAGTACTCTTGATCTTGTCAAATGG 303
 Db 168 oAlaGlnArgProAlaValAlaAla----- 176
 QY 302 CGTCTGT-----CCAGGCGTGGCCCTTGACCAGATGGCGTGTGCTGTACATG 252
 Db 177 -GlyGlyGlnArgGlnProGlyArgAspProAlaGluHisLeuArgProArgArgPro-- 195
 QY 251 CTTCCGCCCTTGATTTGCTCTCTCCGCCAACACAGCAAGCTCATCAACTTGACCTGCTTC 192
 Db 196 -----GlyLeuLeuArgArgProArgArg-----ProAlaG 206
 QY 191 ATCTCTCTCTTGTGATCT-----CCAGGACTCGAAGAAG 156
 Db 206 nProGlyArgLeuAlaSerGlyArgGlyAlaGlyAlaGluProGlySerArgArgAr 226
 QY 155 G-----GCAGCAGC 147
 Db 226 sGlnValProGlyArgArgArgArgPropheArgSerProAlaGlyAlaaspArgAlaVa 246
 QY 146 TCCGGGTGAGCAGCAGCTTATCGTAGAAGTGTCAACCGCCAGCTTCATGCTTCTGCG 87
 Db 246 lProGlyGluProArgProGlyProArgArgArgArgProGluArgProArgArgHi 266
 QY 86 CGCCCCAGGTCTAT---CAACAGCTCTTGGCGCCGATCCGCTTCGCGCTCTCTGTG 30
 Db 266 sArgProAlaHisGlyProGlyAlaGly-TyrProAlaAlaProLeuArgArgAlaGlyG 286
 QY 29 GTGCTGGTGGCGGCTCTGCAGGCGAG 4
 Db 286 lValaThrArgHisArgLeuArgGln 294

RESULT 2

US-09-252-991A-19980
 ; Sequence 19980, Application US/09252991A
 ; Patent No. 6551795

GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 19980

; LENGTH: 170

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-19980

Alignment Scores:

Pred. No.: 5,99e-06 Length: 170
 Score: 134.50 Matches: 68
 Percent Similarity: 38.31% Conservative: 9
 Best Local Similarity: 33.83% Mismatches: 45
 Query Match: 11.99% Indels: 79
 DB: 4 Gaps: 15

US-09-920-953-2 (1-598) x US-09-252-991A-19980 (1-170)
 QY 524 CTGGCGCGCTCGGCAACTGGCGCTCCCGCTCAA-----AATCATGGAATGAGCGC 471
 Db 14 ProGlyArgArgAsnArgArgAlaAlaProAlaAlaAlaGlyArgArgSerAlaArg 33
 QY 470 TCAGGCTGG-----GGTTGGGTTAATGAAATCAGTTGGGTGCGCAGTTGTTGGNAAG 417
 Db 34 SerGlyTTPProCysGlyTTP-----Arg-TTPSerHisProCysTTP----- 47
 QY 416 TCAATTCCTCCGGGTGAGTCCACCACTCCGGGGCGGTGCTGGATCACATCTGCTTG 357
 Db 48 -GlnHisArgArgArgProArgProSerArgArg-----SerArgProAlaAla 64
 QY 356 AGCCCATCTCTTCGAGCGTCTCTCCAAGTACTCTTGTCAAGTGGCGGTGG 297
 Db 64 aArgPro-----SerGlyGlyAla 70
 QY 296 TCCAGCGCTGCCCTTGACAGAT-----GGCGGTGTGCTGTATGATGCTTCGG 246
 Db 70 aAlaileArgArgProValProAspGlyGlnProGlyArgArgArgAsnAlaCys----- 88
 QY 245 CCCTTTGATTGCTGCTCCGCCAACACAGAGCTCATGAACCTTGACCTTCATCTTC 186
 Db 89 -----SerThrArg----- 91
 QY 185 TGCTCTTGCATGCCAGGACTCGA-----AGAAGGCGAGCAGC 147
 Db 92 -----LeuProGlyArgArgArgPheProTrpArgProThrArgArgSerAla 108
 QY 146 TCCGGGTGAG-----CCAGCACCTTATGTAGA-----AG 117
 Db 108 aProGlySerArgThrGluArgAlaProSerProAlaArgArgGlySerArgArgSerAr 128
 QY 116 GTGTCAACCGCCAGCTTCATGCTTCTCGCGCCAGGTCATCAACAGCTTCTTGGCG 57
 Db 128 gArgArgProAlaAla-----ArgArgGlyThrLeuProCysProAlaCysSe 144
 QY 56 CGCATCCCGCTTCGCG-----CGTCTCTGT-----GGTCTGCTGGCGCGCTCTGC 10
 Db 144 r-AlaSerArgAsnArgSerArgSerCysSerArgSerGlySerAlaGlyArgSerCys 163

RESULT 3

US-09-252-991A-30843

; Sequence 30843, Application US/09252991A

; Patent No. 6551795

GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 30843

; LENGTH: 663

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-30843

Alignment Scores:

Pred. No.: 1,12e-05 Length: 663
 Score: 134.00 Matches: 53
 Percent Similarity: 35.71% Conservative: 17
 Best Local Similarity: 27.04% Mismatches: 71
 Query Match: 11.94% Indels: 55
 DB: 4 Gaps: 13

US-09-920-953-2 (1-598) x US-09-252-991A-30843 (1-663)

```

QY 512 CGCAACTCGCGCTCCCGCTCAAAATCGATGG-----AAT 477
Db 45 ArgATGValProIleArgCysAlaAsnAlaTrpProGlyArgProMetSerSerThrSer 64
QY 476 GAGCGCTCAGGCTGGGGT-----TGGGTATATGAAAT 444
Db 65 ArgArgProGlyTrpSerProAlaValProAlaGlyAlaCysCysTrpLysThrArgAsn 84
QY 443 CAGTTGGGTGCGCAGTGTGTGGGNAAGTCAAAATCGTCGCGGGTGAGTCCACACTCCG 384
Db 85 ValAlaGlyArgSerAlaThrAspAlaTrpSerSer-----AlaProAlaPro 100
QY 383 GGGCGGTGCTGATCACATCTGCTTGACGGCCATCTCT-----TCAGGGTCTCT 333
Db 101 AlaAsnCys-----CysCysLeuPheProAlaGlyProSerProAlaSerProAla 117
QY 332 CCAAGGTACTGCTTGATCTTGTTCAAAGTGGCGGTGTCAGGCGG-----TGGCCC 282
Db 118 ProAlaAlaCysArg-----ArgTrpProArgAlaAlaCysHisTrpPro 132
QY 281 TTGACCATAGTGGCGTGTGCGTGTGACANGCTTCGGCCC-----TTGTATTGGTGTCT 228
Db 133 AlaSerAlaTrp-----TrpTrpLeuAlaProAlaArgCysCysTrpProAla 148
QY 227 CGCGCAAAACACGAAGCTCATGAATGACCTTGACCTTCTCTCTCTCTCTCTCTCTCTCAGG 168
Db 149 ProProAla-----ProAlaSerAlaGlyArgAlaCysCysAla 162
QY 167 GACTCGAAGAGGGCAGCAGCTCGCGGTGCAGCCAGCACCTTATCGTAGAGGTGTCAACC 108
Db 162 rProAsnArgA-GArgGluProTrpProProSerProTrpProAlaSerArgAla--G1 181
QY 107 GCACCTTCATGCTTCTTGCGCGCCAGGTTCATCAACAGCTCTTTCGCGCGCATCCC 48
Db 181 yProAlaSerCys-----GlyArgPro-----ProAlaCysSerProValAl 195
QY 47 GCTTCGCGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2
Db 195 aThrAlaProThrAlaThrCysSerProProSerAlaArgSerAla 210

RESULT 4
US-09-252-991A-27249
; Sequence 27249, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEU-
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27249
; LENGTH: 308
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27249

Alignment Scores:
Pred. No.: 1,98e-05 Length: 308
Score: 130.50 Matches: 77
Percent Similarity: 36.59% Conservative: 13
Best Local Similarity: 31.30% Mismatches: 81
Query Match: 11.63% Indels: 75
DB: 4 Gaps: 17
US-09-920-953-2 (1-598) x US-09-252-991A-27249 (1-308)

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US-09-252-991A-29427

Alignment Scores:
Pred. No.: 5, 15e-05 Length: 1476
Score: 129.00 Matches: 74
Percent Similarity: 38.01% Conservative: 10
Best Local Similarity: 33.48% Mismatches: 91
Query Match: 12.09% Indels: 46
DB: 4 Gaps: 13

US-09-920-953-2 (1-598) x US-09-252-991A-29427 (1-1476)

```

QY 9 TCAGAGCGGCGCCACAGACACAGAGAGCGGCGGAGC-----GGGATCGG 56
DB 492 CysArgAlaHisArgGlnHisArgGlnAlaAlaAspAlaLeuGlyGlnArg 511
QY 57 GCGCAAGAGCTGTTGATGACTGGCGGCGGAGAGGCATGAAGCTGGCGGTGACAC 116
DB 512 ThrGlnLeuSerArg--ArgProGlyGlnLeuArgAlaProGlyHisArgAlaHis 530
QY 117 CTTCTACGATAAGTGGCTGAGCCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 176
DB 531 LeuProGlnLeuGlyAlaAla--ValGlyGlyAlaGlyLeuArgArg-----GlyHis 547
QY 177 GCAAGAGCAGAGATGAAGAGGCTCAAGTTCATGAGCTTCGTGTTGGCGAGCAGACCA 236
DB 548 ArgProGlyArgTrpProValGlyLeuValArg-----ArgArgLeuPro 562
QY 237 ATA-----CAAGGCGCGAAGCATGTACAGCCACAGCCCATCTGTCAAGCGCCACGG 290
DB 563 AlaGlyArgGlyThrArgArgGlnGlyThrArgArgGlnGlyThrArgArgProGlyProAla 582
QY 291 CTGGA-----CCACGGCA-----CTTTCACAGATCAAGCAGTA 326
DB 583 ProGlyAlaGlyAlaAspArgProProAlaPheLeuLeuSerGlyAlaAlaArg 602
QY 327 CTTTGGAGAGCGCTGCAAGAGATGGCGTCAA-----GCAGGATGTGATCCAGCAGCG 380
DB 603 Pro--ArgArgAlaGlyProAspArgGlnProProAlaGlyProAspProGlyArg 621
QY 381 CCGCGAGTGTGGAGTCAACCGC-----GACGAATTGACTNCCCAACAA 428
DB 622 ArgHisArgGlyAlaVal--ThrArgCysGlyAlaGlyThrGluAlaGlyValProArgPr 641
QY 429 CTGCGACCAACTCATTTTCATTAAACCAACCCAG----- 465
DB 641 OProGlnProAlaAspGlyAlaThrAlaAlaAspGlnGlnGlyArgAspProGlySerHi 661
QY 466 -----CTGAGCGCTCATTCATCGATTTTGGAGCGGAGCGCCAGTTCGCGAGCGCGCC 521
DB 661 sProProGlyArgAspAlaArg-----AlaThrValArgProArgPr 676
QY 522 AGGGGCGCAGAGCGCTGCAATCTGTTGCCAGCCCTGCTGCTGCTGCTGCTGCTGCTG 580
DB 676 OserArgProAlaGly--GlnTyHisProProAlaArgValAlaGlyLysArgHisArg 695

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RESULT 6

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US-09-252-991A-24046
; Sequence 24046, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 24046

```

; LENGTH: 235

; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-24046

Alignment Scores:
Pred. No.: 5, 38e-05 Length: 235
Score: 126.00 Matches: 47
Percent Similarity: 39.16% Conservative: 18
Best Local Similarity: 28.31% Mismatches: 58
Query Match: 11.23% Indels: 43
DB: 4 Gaps: 10

US-09-920-953-2 (1-598) x US-09-252-991A-24046 (1-235)

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QY 482 TGAATAGCGCTCAGGC---TGC-----GGTTGGTTAATGAAATCAG 441
DB 26 TrpAspGlyArgSerGlyArgTrpSerArgArgTrpCysAlaTrp----- 40
QY 440 TTGGGTGCGCAGCTGTGGGNAAGTCAAAATTCGTGCGGTGGACTCCACACATCCGGCG 381
DB 41 ---GlyCysProSerValAlaProThrArgTrpSerArgGlyCysSerArgSerProPro 59
QY 380 GCGTGTGGATCACATCTCTGACGCCATCTCTTGCGCGCTCTCTCCAGGTACTGC 321
DB 60 CysAlaTrpAlaSerSerAlaIleThrProTrpProArgThrArgSerProSer----- 77
QY 320 TTGATCTTCAAGTGGCGGTGCTCCAGCGCTGCTGACCATGATGGCGGTGCG 261
DB 78 -----ArgArgTrpTrp---ArgSerTrp-----CysArgTrpGlyCysArg 91
QY 260 TCGTACATCTTCGGCCCTTGATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 201
DB 92 -----ThrProProPro-Thr----- 96
QY 200 ACTGCTTCTATCTTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 141
DB 97 -----AlaSerAlaSerIleSerAlaProAlaAlaCysSerLysHisAlaAlaProGI 114
QY 140 TCAGCCAGCACCTTATCGTAGAAGGTGT-----CAACCGCCAGCTTCATGCT 93
DB 114 yValSerAlaSerAlaSerAlaArgCysAlaCysCysSerSerProGlySerSerGlyGI 134
QY 92 TGTGCGCCCGCAGGTATCAACAGCTTCTTGGCCCGCATCCCGCTTCGCGCTCTCT 33
DB 134 yCysArgArgProSerSerAlaCysSerSerThrAla---ThrProArgProThrGlyAr 153
QY 32 GTGGTCTGCTGGCGG 17
DB 153 gtrpProArgtrpPro 158

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RESULT 7

```

US-09-252-991A-19344
; Sequence 19344, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 19344
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-19344

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; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 20675
; LENGTH: 726
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20675

Alignment Scores:
Pred. No.: 0.000219 Length: 726
Score: 122.00 Matches: 74
Percent Similarity: 32.13% Conservatives: 6
Best Local Similarity: 29.72% Mismatches: 74
Query Match: 11.43% Indels: 95
DB: 4 Gaps: 13

US-09-920-953-2 (1-598) x US-09-252-991A-20675 (1-726)
QY 2 CGCTCCCTGCAGAG-----CGGCCACACACACAGACGCGCGGAGCGGATGCG 55
Db 299 ArgAlaLeuArgThrGluArgHisProProAspProGlyArgHis-GlyProProAlaAr 318
QY 56 GCGCAAGAAGCTGTTTCATGACCTGGCGCGCGAGAG-----CATGAAGC 103
Db 318 g-----ProAlaAlaArgArgAlaAlaValGlyGluAl 331
QY 104 TGGC-----GGTTGACACCTTCTACGATAGTCTGCG-----TGACCGGAGC 148
Db 331 aglyAlaAlaGlyGlnGlyProArgThrGlyAlaAlaArgThrGlnSerProGly: 351
QY 149 TGCTCCCTTCCTGAGTCCCTGGACATGCAAGAGCAGACAGTGAAGCAGGTCAAGTTCA 208
Db 351 rAlaGlySerAlaAlaLeuArgAlaHisArgArgAlaGlySerAla-----AlaGl 369
QY 209 TGAGCTTCGTGT-----TGG----- 224
Db 369 yGluLeuArgAlaArgProGlyProTrpProAlaAlaGlnGlnProAlaSerAlaAlaPr 389
QY 225 -----CGGAGCAGACCAATACAGG 244
Db 389 cAlaProGlyGluGlyArgGlyThrAlaArgAlaAlaArgArgGlnAlaAlaArgGlnAr 409
QY 245 GCGAAGCATGTACGACGACACACGCCATCTGTTCAAGGGCCACGGCTGGACACCGCC 304
Db 409 gProThrAlaValArgThrAspArgGluAspGlnGlyArgProArgProProPr 429
QY 305 ACTTTGACAA-----GATCAA-----GCAGTACTTGGAGAGCGCTGCAAG 346
Db 429 oProAlaGlnProGluAspGlnProAlaProAlaAlaProGlyArgAspAlaAlaAr 449
QY 347 AGAT----- 350
Db 449 gAspAspProGlnArgThrHisGlyThrAlaProAlaGluGlyAlaAlaGlnProGlnAr 469
QY 351 -----GGCGTCAAGCAGGATGTATCCACACGCGCGGAGTGTGAGT 397
Db 469 gGlnProAspHisGlyArgHisGlnProGlyAspProGlyValLeuProArgGlyAl 489
QY 398 CCACCGGACGAATTTGACTTNCACCAACTGGCCACCACTGATTTTCATTAAACC 457
Db 489 aArgProArg-----GlnProArgAlaArgGlyArgHisGlyGlnPr 503
QY 458 AACCCCGAGCTGAGCGCTCATTCATTCGATTTTGTAGCGGGAGCGCCAGTTGCCAGGCG 517
Db 503 o-----HisGlyArgArgHisLeuProProAl 512
QY 518 GCCCAGGGGGCCAGGAGCTGCAA 542

Db 512 aGlnArgGlyGluProAlaLeuArg 520

RESULT 10
US-09-252-991A-17837
; Sequence 17837, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17837
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17837

Alignment Scores:
Pred. No.: 0.000154 Length: 204
Score: 121.50 Matches: 60
Percent Similarity: 34.56% Conservatives: 15
Best Local Similarity: 27.65% Mismatches: 77
Query Match: 11.39% Indels: 65
DB: 4 Gaps: 14

US-09-920-953-2 (1-598) x US-09-252-991A-17837 (1-204)
QY 5 TGCTCTCAGACGCGGCCACACACACAGACGCGCGGAGTGGCGGCCAAGA 64
Db 7 CysSerSerThrArgProProThrTrp-----ProSerAlaAsn 21
QY 65 ACTGTGTTTCATGACCTGGCGCGCGAGGAGCATGAAGCTGGCGTTCACACCTTCTACG 124
Db 22 SerMetAlaThrAlaTrpProProPheProAlaAlaSerTrpArgArgThr-----Thr 39
QY 125 ATAAGTGTCTGG-----CTGACCCGCGAGCTGC----- 151
Db 40 SerArgCysCysAlaProAlaThrAspArgSerCysSerThrAlaThrSerGlyIleArg 59
QY 152 TGCCCTTCTTCAGTCCCTGGACATGCAAGACAGACAGATGAAGCAGGTCAAGTTTCATGA 211
Db 60 CysGlyThrSerArgProTrp---AlaGlySerArgProProProArgSerSer----- 76
QY 212 GCTTCGTGTTTGGCGAGCAGACCAATACAGGGCGCGAGCATGTACGACGACACGCC 271
Db 77 -----ArgGluProGluProCys-----ArgAlaPro 85
QY 272 ATCTGTCAAGGCCACGCGCTTGGACCCACCGCCATTTTCACAGATCAAGCAGTACCTTG 331
Db 86 ProTrpSer-----AlaAlaTrp-----AlaAlaThrCys 95
QY 332 GAGAGACGCTGCAAGAGATGGCGGTCAAGCAGGATGTATCCAGCAGCGCGCGGAGTGG 391
Db 96 ProArgProCysSerAlaThrThrCysSer-----ProProSerTrp 109
QY 392 TGGAGTCCACCGCGCAGAAATTTGACTTNCACCAACTGCGCACCCCACTGATTTTCAT 451
Db 110 ThrLeuProThrProGlySerAlaAlaProAlaCysAlaSerGlyIle----- 126
QY 452 TAACCCCAACCCAGCGCTGAGCGCTCATTCATCGATTTTGTAGCGGGAGCGCGCAGTT--- 508
Db 127 -----SerProAlaThrSerAla---AlaAlaThrTrpProCysGlyArgProPro 143
QY 509 -----GCCGAGCGCGCCAGGGGGCCAGAGCCTCAATCGT 547
```

Db 144 ArgSerProArgArgGlyTyrSerGluSerMetArgTyrCysTyrGlnProAla----- 161
QY 548 TTGCAGCCCTTGTGCTAATGAAGCATCAGCATTTTGGCACCAGCC 598
Db 162 ---ProAlaThrSerAlaAlaArgProProArgProGlySerArgAla 177
RESULT 11
US-09-252-991A-18476
; Sequence 18476, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18476
; LENGTH: 351
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18476
Alignment Scores:
Pred. No.: 0.000188 Length: 351
Score: 121.50 Matches: 58
Percent Similarity: 33.50% Conservative: 10
Best Local Similarity: 28.57% Mismatches: 58
Query Match: 11.39% Indels: 77
Gaps: 10
DB: 4
US-09-920-953-2 (1-598) x US-09-252-991A-18476 (1-351)
QY 30 CACAGACGCGGAGCGGATCGCGGCGCAGAACCTTTGATGACCTGGCGGCGCC 89
Db 131 HisArgAlaAlaGlyArgGlyProAlaAlaGlyProSerGlyProArgProGlyArgGat 150
QY 90 AGA-----AGCATGAAGCTGGCGGTTGACACCTTCTACGATAAGGT 131
Db 151 LysProAlaValArgProAlaAlaArgHisAlaAlaProAla----- 163
QY 132 GCTGGTCACCGGAGCTGCTGCCCTTCTTCGAGTCCCTGGA-----CATGCA 179
Db 164 -----ProGlyLysAspProArgArgArgArgGlyAspGlnGluProHisArg 180
QY 180 AGACGACAGATGAAGCAGCTCAAGTTTCATGAGCTTGTGTTGGCGGACGACCAATA 239
Db 181 AlalaArgArgAlaGlyGlyAlaHis-----ArgProTyrArg-----ArgProLeu 197
QY 240 CAAGGCGCGGAGCATGTACGACGACGACGACGACGACGACGACGACGACGACGACGAC 299
Db 198 ProGlyProAspHisProArgGlyGlyGlnProAlaGlyGlyLeuProHisAla----- 215
QY 300 CCGCCATTTCACAGATCAAGCATCAAGTACCTTTGGAGAGACGCTGCAAGAGATGGCGTCAA 359
Db 216 -----AlaileArgArgGlyArgGln 222
QY 360 -----CGAGGATGTATCCAGCA-----CGCCGCGCG 386
Db 223 AlaLeuArgAlaGlyArgGlnProAlaProAspArgProLeuHisArgArgArgArgG 242
QY 387 AGTGGTGGATCCACCGCAGCAAGATTGACTTTCCTTCCCACTGCGCACCCTGATT 446
Db 243 ProGlyAlaValAlaProAlaAlaArgLeuGlyAsnLeuAlaGlyGlnAlaGln----- 260
QY 447 TTCATTAAACCAACCCAGCGCTGAGCGCTCATTCCTGATTTTGGCGGGAGCGCCAG 506
Db 261 -----GlyArgArgAla 264

QY 507 TTGCCG-----AGCGCCCGCAGGCGGCGCCAGGAGC 536
Db 265 GlyProArgArgArgAlaAlaArgHisLeuA-gProProArgArgProArgArg 284
QY 537 CTGCAATC 545
Db 285 LeuArgVal 287
RESULT 12
US-09-252-991A-20161
; Sequence 20161, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 20161
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20161
Alignment Scores:
Pred. No.: 0.000187 Length: 248
Score: 121.00 Matches: 47
Percent Similarity: 35.11% Conservative: 19
Best Local Similarity: 25.00% Mismatches: 62
Query Match: 11.34% Indels: 60
Gaps: 4
DB: 4
US-09-920-953-2 (1-598) x US-09-252-991A-20161 (1-248)
QY 2 CGCTCGCTGCAGACGCGGCGCACACCA-----CACAGACGCGCGGAGCGGATCGGCGC 58
Db 56 ArgCysAlaArgSerProProAlaGlyProSerSerThrThrArgArgProAlaSer 75
QY 59 GCAAGA---AGCTGTTTGTATGACCTGGCGGCGGAGAGGATGAAGTGGCGGTTGACA 115
Db 76 AlaSerIleArgCys-----SerAlaArgValArgLysTyrTrpSerThr 90
QY 116 CTTTCTACGATAAGC----- 130
Db 91 SerAlaThrIleArgLysAsnSerAlaAlaAsnThrLysAlaAlaArgArgTrpCysArg 110
QY 131 -----TGCTGCTGACCGCGAGC-----TGCTGC----- 154
Db 111 ArgCysAlaCysTyr-----ThrArgAsnArgProAlaArgSerCysArgCysValala 129
QY 155 -----CCTTCTTCAGTCCCTTGGACATGC 178
Db 130 ThrArgSerSerAlaProProThrThrProAlaProThrSerIleProThrProCys 149
QY 179 AAGACGACAGATGAAGCAGGTCAAGTTCATGAGCTTCGTTGGCGGAGCAGACCAAT 238
Db 150 ThrArg-----AlaThrCysAlaAlaSerAlaAla----- 159
QY 239 ACAAGGCGCGAAGCATGTACGACGACGACGACGACGACGACGACGACGACGACGACG 298
Db 160 ThrArgGlyArgSerCysAlaThr-----ThrLysArgTyrArgSerAlaGlySerThrAla 178
QY 299 ACCGCCATTTCACAGATCAAGCAGTACCTTGGAGAGACGCTGCAAGAGATGGCGTCA 358
Db 179 ProGlyLysSerAlaAlaThrProAlaThrThrAlaArgArgCys-----TrpSerThr 196

QY 359 AGCAGGATGTCATCCAGCAGCCGCGGAGTGGTGGAGTCCACCCGCGACGAATTTGACT 418
 Db 197 ProGlnAlaProGlyAlaThrProSerProGlyTrpProAlaSerAlaArgTrpAlaCys 216
 QY 419 TWCCCAACACTGCCACCAACT 442
 Db 217 SerProSerAlaAlaGlnProSer 224

RESULT 13

US-09-252-991A-20509
 ; Sequence 20509, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 20509
 ; LENGTH: 686
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-20509

Alignment Scores:
 Pred. No.: 0.000274 Length: 686
 Score: 121.00 Matches: 51
 Percent Similarity: 35.22% Conservative: 5
 Best Local Similarity: 32.08% Mismatches: 47
 Query Match: 11.34% Indels: 56
 DB: 4 Gaps: 9

US-09-920-953-2 (1-598) x US-09-252-991A-20509 (1-686)

QY 3 GTCGCTGACAGCGCGCCACGACGACGACGAGCGCGGAGCGGATCGCGCGCAA 62
 Db 117 AlaAlaCysArgGlyAlaTrpHis-----GlyLeuArgProArg 130
 QY 63 GAAGTGTGTTGATACCTGGCGCGCGCAGAGGATGAAGCTGGCGTTGACACCTTCTA 122
 Db 131 ProAla-----GlyArgArgArgArgProAlaAlaGlyGly----- 142
 QY 123 CGATAAGTGTGCTGACCGCGAGCTGCTGCCCTTCTTCAGATCCCTGGACATGCAAGA 182
 Db 143 -----GlnArgTyrAlaAlaGluArgCysAlaGlyLeuAlaArg 155
 QY 183 GCAGAAGATGAACAGGTCAAGTTCATGAGTTCGTGTTGG----- 224
 Db 156 ProAlaProArgThr-----ValAlaArgArgArgProTrpArgHisProArgCysAla 173
 QY 225 -----CGGAGCAGACCAATACAGCGCGCGAGCATGTACGACGACACGCGCATCTGGT 278
 Db 174 ValProArgGlyArgProAlaAlaGlyAla-----AlaAlaArgArgGlyAlaGly 191
 QY 279 CAAGGCCACGCTGGACCGCCACTTTGACAGATCAAGCAGTACCTTGGAGAGAC 338
 Db 192 GlyGlyIleGlnProGlyLeuPro-----CysLeuAlaTrpArgAla 205
 QY 339 GCTGCAAGA-----GATGGCGGTCAA 359
 Db 206 AlaAlaArgGlyLeuAlaArgLeuProProGlyGlnProTrpAlaThrGlyAlaArgGln 225
 QY 360 GCAGTATGTATCCAGCAGCGCGCGAGTGTGA-----GTCACCGC 404
 Db 226 ProGlyAlaGlyAlaGlyProArgGlyGlyGlyValArgArgThrHisPro 244

RESULT 14

US-09-252-991A-23215
 ; Sequence 23215, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 23215
 ; LENGTH: 219
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-23215

Alignment Scores:
 Pred. No.: 0.000228 Length: 219
 Score: 120.00 Matches: 57
 Percent Similarity: 38.27% Conservative: 18
 Best Local Similarity: 29.08% Mismatches: 72
 Query Match: 10.70% Indels: 49
 DB: 4 Gaps: 9

US-09-920-953-2 (1-598) x US-09-252-991A-23215 (1-219)

QY 593 GGTGCGAAAATGGCTGATGGCTTCAATGACAGGAGGCTGGCAAAACGATTTCAGGCT 534
 Db 58 GlyArgArgTyrSerAspArgSerAlaPro-----AlaAsnProProGly 73
 QY 533 CTGCGCCCGCTGGCGCGCTGGCACTGGCGCTCCCG-----GCTCAAAATCGA 483
 Db 74 ProGlySerValProArgSerArgArgTyrAlaValProGlyAlaAlaArgSerArg 93
 QY 482 TGAATGAGCGCTCAG-----GCTGGGGTTGGTTAATGAAATCAGTTGGT 435
 Db 94 -ProAlaThrGlyProProProArgTrpAlaGlyProGlyHisArgAlaAlaAlaTrpLe 113
 QY 434 GGCACATTGTTGGGNAAGTCAAAATCGTCGGGTGGACTCCACCACCTCCGCGCGTGC 375
 Db 113 uA-g-----ArgArgAlaSe 118
 QY 374 TGGATCACATCTGCTTGACGCCATCTCTTGAGCGCTCTCTCCAAGGTACTGCTTGATC 315
 Db 118 rAlaSerCysProGlyHisArgGlyAspSerGlySerSerProGlyProArgLysAl 138
 QY 314 TTCTCAAGTGGCGGT-----GGTCAGCGCTGGCCCTTACACGATGGCGGTGT 264
 Db 138 aThrArgGlyHisGlyArgLysArgProGlyArg-----ProAspAlaProVa 155
 QY 263 GCGCTGTACATGCTTCGGCCCTTGATTGTTGCTGCTCCGCAAAACACGAAGCTCATGAAC 204
 Db 155 lA-gA-g-----AlaProAlaAsnSerVal----- 163
 QY 203 TTGACCTGCTTCACTTCTGCTCTTCATGTCGAGGACTCGAAGAGGCGGCGAGCTCC 144
 Db 164 ----ProAlaSerArgGlyArgAlaGlyCysSerArgPheArgCysArgThrProAlaPr 182
 QY 143 GGTCTACGACGACCTTATCGTAGAGGTGTCAACCGCAGCTTCATGCTTCTCGCGCG 84
 Db 182 oGlyAlaProAlaArgProAlaGlyArgArgSerProProAlaArgCys-----Ar 199
 QY 83 CCCAGGTTCATCAACAGCTTCTTCGCGCGGATCCCGCTTCGCGCG 38
 Db 199 gSerGlyCysAlaAlaAlaArgGlyProProValProValProPro 214

RESULT 15

US-09-252-991A-24725

; Sequence 24725, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 24725
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24725

Alignment Scores:
Pred. No.: 0.000253 Length: 209
Score: 119.50 Matches: 55
Percent Similarity: 33.04% Conservative: 19
Best Local Similarity: 24.55% Mismatches: 73
Query Match: 10.65% Indels: 77
DB: 4 Gaps: 11

US-09-920-953-2 (1-598) x US-09-252-991A-24725 (1-209)

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QY 497 CCGGCTCAAAATCGATGAATGAGCGCTCAGGCTGG-----GGTTGG 456
Db 5 ProThrArgArgSerAlaAlaArgSerTrpSerAlaAlaArgSerAlaGlyTrp 24
QY 455 GTTAATGAATCATGTTGGTGGCAGTTG-----TTGGNAAGTCMAATTCGTG 405
Db 25 LysProArgThrIleProGlySerArgSerAlaThrGlyTyrSerArgProThrAlaGly 44
QY 404 CGGTGGGACTCCACACTCCGCGCGGTGGTGCATCATCTGCTTG----- 357
Db 45 ArgThrThrArgPheProThrAlaAlaAlaTrpArgAlaTrpAlaSerArgSerIle 64
QY 356 -----ACGCCATCTTGTGAGCGTCTCTCCAAAGTACTGCTTGTATCTTCAAGTGG 303
Db 65 ArgProThrProTrpAlaCysSerAlaCysProala----- 76
QY 302 CGGTGGTCCAGCGCTGCGCCCTTGACACAGATGGCGGTGCTGCTATATG----- 252
Db 77 -----SerProPro-----ThrTrpAlaCysSerThrSerAlaSerProArg 90
QY 251 ---CTTCGCGCCTTGTATTGTCTGCTCCGCCAAACACGAAGCTCATGACTTGCCT-- 197
Db 91 ProAlaArgProTrpTrpTrpProProProGly-ArgSerAla-----ProPr 107
QY 196 -----GTTTCATCTTCTGCTCTT-----GCATGTCAGGAGTCTGAAG 159
Db 107 oSerAspArgSerAlaSerArgAlaAlaGluTrpSerAlaSerProAlaValArgLy 127
QY 158 AAGGCACAGCTCCGGGTGAC----- 137
Db 127 sasnAlaAlaThrProCysArgCysSerAlaSerMetProAlaSerThrThrMetProAr 147
QY 136 -----CCAGCACCTTATCGT----- 122
Db 147 gThrSerProAsnAspTrpProArgProAlaArgThrAlaSerThrSerIleThrArgth 167
QY 121 -----AGAGGTCTCAACCGCAGCTTCATGCTTCTGCGCGCCCGAGGTCACTCA 72
Db 167 rSerAlaAlaArgSerThrProSerArgCysSerThrProArgProGlySerAr 187
QY 71 AACAGCTTCTTGGCCCGCATCCCGCTTCCGCGCTCTCTGTGTGCTGTGGCGCGCTCT 12
Db 187 gSerAlaAlaSerProThrThrThrThrProSer-CysHisProGlyArgThrAlaC 207
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QY 11 GCAGGCAG 4
Db 207 ysArgArg 209

Search completed: July 19, 2004, 17:20:42
Job time : 24 secs

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OM nucleic - protein search, using frame_plus_n2p model

Run on: July 19, 2004, 17:19:11 ; Search time 46 Seconds
(without alignments)
8126.576 Million cell updates/sec

Title: US-09-920-953-2

Perfect score: 1067

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1285345 seqs, 312560633 residues

Total number of hits satisfying chosen parameters: 2570690

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=Published Applications AA -QFMT=fastan -SUFFIX=rapb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNIT5=bits -START=1 -END=1 -MATRIX=DIOSUM62
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-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
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-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications AA:

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pcp.*
- 2: /cgn2_6/ptodata/2/pubpaa/pct_NEW_PUB.pcp.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pcp.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pcp.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pcp.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pcp.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pcp.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pcp.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pcp.*
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- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pcp.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pcp.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pcp.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pcp.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pcp.*
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- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query Match Length DB ID Description

RESULT 1
US-10-282-122A-61519
; Sequence 61519, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848

ALIGNMENTS

1	254.5	23.9	124	12	US-10-282-122A-61519
2	148	13.9	324	12	US-10-425-114-58160
3	142.5	13.4	19723	15	US-10-084-846A-5
4	125	11.7	417	16	US-10-437-963-143835
5	125	11.7	19695	15	US-10-084-846A-3
6	124.5	11.1	19662	15	US-10-084-846A-6
7	120.5	11.3	19608	15	US-10-084-846A-8
8	119.5	11.2	276	16	US-10-437-963-166380
9	117.5	11.0	384	12	US-10-425-114-72136
10	117.5	11.0	384	12	US-10-425-114-72137
11	117.5	10.5	19723	15	US-10-084-846A-5
12	116.5	10.4	19652	15	US-10-084-846A-7
13	115.5	10.3	155	16	US-10-437-963-103601
14	115.5	10.8	224	16	US-10-437-963-141171
15	115.5	10.8	517	12	US-10-425-114-63797
16	115.5	10.8	517	12	US-10-425-114-63798
17	115.5	10.8	517	12	US-10-425-114-63800
18	115.5	10.8	728	12	US-10-425-114-63691
19	114.5	10.7	381	12	US-10-425-114-47573
20	114.5	10.7	401	12	US-10-425-114-40384
21	113.5	10.6	398	12	US-10-425-114-46621
22	112	10.5	247	12	US-10-425-114-48205
23	112	10.5	19725	15	US-10-084-846A-4
24	111	9.9	265	16	US-10-437-963-176482
25	110.5	10.4	294	16	US-10-437-963-106950
26	110.5	10.4	492	12	US-10-425-114-65735
27	109.5	10.3	530	12	US-10-425-114-65735
28	109.5	10.3	19662	15	US-10-084-846A-6
29	109	9.7	110	16	US-10-437-963-168168
30	109	10.2	273	12	US-10-425-114-64278
31	109	9.7	354	12	US-10-425-114-57426
32	109	9.7	19695	15	US-10-084-846A-3
33	108.5	10.2	312	12	US-10-425-114-61224
34	108.5	10.2	383	12	US-10-425-114-61224
35	107.5	9.6	337	12	US-10-425-114-53493
36	107.5	10.1	397	16	US-10-437-963-128400
37	107	10.0	437	16	US-10-437-963-132079
38	107	9.5	19725	15	US-10-084-846A-4
39	106.5	9.5	336	12	US-10-425-114-56601
40	106	9.4	320	12	US-10-425-114-70729
41	106	9.4	490	16	US-10-437-963-104973
42	105.5	9.9	223	12	US-10-425-114-38596
43	105.5	9.4	19608	15	US-10-084-846A-8
44	105	9.8	285	12	US-10-425-114-50473
45	104.5	9.8	199	16	US-10-437-963-126060

Sequence 61519, A
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Sequence 141171,
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Sequence 4, Appli
Sequence 176482,
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Sequence 65735, A
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Sequence 61224, A
Sequence 53493, A
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Sequence 132079,
Sequence 4, Appli
Sequence 56601, A
Sequence 70729, A
Sequence 104973, A
Sequence 38596, A
Sequence 8, Appli
Sequence 50473, A
Sequence 126060,

; PRIOR FILING DATE: 2000-05-23
 ; PRIOR APPLICATION NUMBER: 60/207,727
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: 60/230,335
 ; PRIOR FILING DATE: 2000-09-06
 ; PRIOR APPLICATION NUMBER: 60/230,347
 ; PRIOR FILING DATE: 2000-09-09
 ; PRIOR APPLICATION NUMBER: 60/242,578
 ; PRIOR FILING DATE: 2000-10-23
 ; PRIOR APPLICATION NUMBER: 60/253,625
 ; PRIOR FILING DATE: 2000-11-27
 ; PRIOR APPLICATION NUMBER: 60/257,931
 ; PRIOR FILING DATE: 2000-12-22
 ; PRIOR APPLICATION NUMBER: 60/267,636
 ; PRIOR FILING DATE: 2001-02-09
 ; PRIOR APPLICATION NUMBER: 60/269,308
 ; PRIOR FILING DATE: 2001-02-16
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 78614
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 61519
 ; LENGTH: 124
 ; TYPE: PRT
 ; ORGANISM: Legionella pneumophila
 ; US-10-282-122A-61519

Alignment Scores:
 Pred. No.: 1,49e-15 Length: 124
 Score: 254.50 Matches: 49
 Percent Similarity: 64.10% Conservative: 26
 Best Local Similarity: 41.88% Mismatches: 41
 Query Match: 23.85% Indels: 1
 DB: 12 Gaps: 1

US-09-920-953-2 (1-598) x US-10-282-122A-61519 (1-124)

QY 61 AAGAGCTGTTGATGACTGGCGCGCAGAGGATGAGCTGGCGGTGACACCTTC 120
 Db 3 GluSerLeuPheGluArgLeuGlyGlnAsnAlaValAsnThrAlaValAspPhe 22
 QY 121 TACGATAAGCTCTGGCTGACCGGAGCTGCTGCGCTTCTCGAGTCCCTCGACATGCAA 180
 Db 23 TyrArgLysMetLeuMetAspArgValAsnTyrPhePheAspValAspMetGlu 42
 QY 181 GAGCAGAGATGAACAGCTCAAGTTGATGAGCTTCTGTTGGCGGAGCAGACATAC 240
 Db 43 GlnGlnLeuLysGlnLysGlyPheLeuThrMetValPheGlyGlyProAsnGlnTyr 62
 QY 241 AAGGCGGAAGATGATGACGACACACCCATCTGTCAGGCGCAGGCTCGACAC 300
 Db 63 ThrGlyLysSerMetArgGluGlyHisGlnHisLeuLeu---AlaArgGlyLeuAsnAsp 81
 QY 301 CCCACTTTGACAGATCAAGCAGTACCTTGAGAGACGCTGCAAGAGATGGCGTCAAG 360
 Db 82 SerHisValAspIleValIleGluHisLeuGlyGluThrLeuLysGluLeuGlyAlaAsn 101
 QY 361 CAGGATGTATCCACACCGCGGAGTGTGGAGTCCACCCCGCAGCAA 411
 Db 102 GluGluAspIleGlnLysValAlaAlaIleAlaAsnSerValArgGlyAsp 118

RESULT 2

US-10-425-114-58160
 ; Sequence 58160, Application US/10425114
 ; Publication No. US20040034888A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Jingdong
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Screen, Steven E.
 ; APPLICANT: Tabaska, Jack E.
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53313)B
 ; CURRENT APPLICATION NUMBER: US/10/425,114
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 73128
 ; SEQ ID NO 58160
 ; LENGTH: 324
 ; TYPE: PRT
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: UC-ZMFLB73219F07_FLI pep
 ; US-10-425-114-58160

Alignment Scores:
 Pred. No.: 2.9e-05 Length: 324
 Score: 148.00 Matches: 62
 Percent Similarity: 38.10% Conservative: 18
 Best Local Similarity: 29.52% Mismatches: 77
 Query Match: 13.87% Indels: 53
 DB: 12 Gaps: 10

US-09-920-953-2 (1-598) x US-10-425-114-58160 (1-324)

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 Db 84 CysAlaArgThrArgAlaArgThrThrAlaProSerAlaProCysThrArgArgThr 103
 QY 50 GATCGGGCGGCAAGAGCTGTTGATGACCTGGCGGCGCAGAGGCATGAAGCTGGCGG 109
 Db 104 SerSerGlySerArgAlaCys-----110
 QY 110 TTGACACCTTCTACGATAAGGTGCTGG-----CTACCCGGAGCTGTGTC 154
 Db 111 -----ProSerAlaAlaThrCysTrpArgTrpAlaAlaThrArgSerArgProThrSer 128
 QY 155 CTTTCTTCGAGTCCCTGGACATGCAAGACGACAGATGAAGCAGGTCAAGTTTCATGAGCT 214
 Db 129 ProArgTrpGlyProTrpCysCysProSerProSer---SerCysSerSerSerArgAla 147
 QY 215 TGTGTTTCGGGAGCAGACCAATACAGGGCGGAGCATGTACGACGACACGCGCCATC 274
 Db 148 CysCysSerAlaThrCysSerArgProArg-ProProArgArgArgArgArgProGln 167
 QY 275 TGTG-----CAAGGCCACGCGCTGGACCCGCGCCTTTGACAGATCAAGCAGTACC 328
 Db 167 nGlyThrProArgProProArgPro--ThrSerArgThrSerSerAlaArgSerThr 186
 QY 329 TTGAGAGACGCTGCAAGAGA-----TGGCGCTCAAGCAGGATGTGATCC 373
 Db 187 -----SerAlaCysThrArgProAlaAlaThrCysTrpSerThrCysArgAlaThrTrp 204
 QY 374 AGCACCGCCCGGAGTGTGGAGTCCACCGCGGACGAATTTGACTTCCCACTGCGG 433
 Db 205 AlaCysAlaThrProThrTrpArgProProAlaProArgCysThrAlaSerAlaThr--- 223
 QY 434 CACCCAACTGATTTTCATTAAACCCACCCAGCCCTGAGCGCTCATTCCTCAATTTTGA 493
 Db 224 -----ProGlnAlaAlaAlaSerGlyThrSerTrpArg 234
 QY 494 -----CGGGAGCGCGAGTTCGCGAGCGCGCCAGGCGGCGGCGGCGGAGGCTGCA 541
 Db 235 ThrTrpArgProArgAlaAlaSerAlaAlaAlaThrAlaSerGlySer---SerProSer 253
 QY 542 AATCGTTTCCGACCGCTTCTGCA 565
 Db 254 GlyArgAlaSerSerAlaThrAla 261

RESULT 3

US-10-084-846A-5
 ; Sequence 5, Application US/10084846A
 ; Publication No. US20040006026A1
 ; GENERAL INFORMATION:
 ; APPLICANT: WEITNAUER, GABRIELE
 ; APPLICANT: MUHLENWEG, AGNES

Db 128 SerProSerThrProSerAlaAlaProSerThrSerSerProThrArgAlaSerProPro 147
 QY 458 AACCCAGCCTGAGCGCTCATTCATCGATTGTGAGCGGAGCGCCAGTTCGCGAGCGC 517
 Db 148 TyrArgSerThrSerProSerProPro--ProAlaAlaSerSerAlaAlaAla 167
 QY 518 GCCAGGGGGGCCA-----CGAGCCTGCAAAATCGTTTG 550
 Db 167 TgProProAlaProThrThrSerProThrArgProProSerGlyCysAlaSerLeuA 187
 QY 551 CGAGCCTTGTGCTGATTAAGAGCCA 576
 Db 187 laThrProAlaThrThrSerThrPro 195

RESULT 5
 US-10-084-846A-3
 ; Sequence 3, Application US/10084846A
 ; Publication No. US20040006026A1
 ; GENERAL INFORMATION:
 ; APPLICANT: WEITNAUER, GABRIELE
 ; APPLICANT: MUHLENWEG, AGNES
 ; APPLICANT: TREPZER, AXEL
 ; APPLICANT: BECHTHOLD, ANDREAS
 ; TITLE OF INVENTION: AVILAMYCIN DERIVATIVES
 ; FILE REFERENCE: 1974-005
 ; CURRENT APPLICATION NUMBER: US/10/084,846A
 ; PRIOR FILING DATE: 2003-02-25
 ; PRIOR APPLICATION NUMBER: PCT/EP01/09815
 ; PRIOR FILING DATE: 2001-08-24
 ; PRIOR APPLICATION NUMBER: DE 101 09 166.4
 ; PRIOR FILING DATE: 2001-02-25
 ; NUMBER OF SEQ ID NOS: 120
 ; SOFTWARE: PatentIn Ver. 3.2
 ; SEQ ID NO 3
 ; LENGTH: 19695
 ; TYPE: PRT
 ; ORGANISM: Streptomyces viridochromogenes
 ; FEATURES:
 ; OTHER INFORMATION: Protein 1: amino acid sequence encoded by coding strand 1.
 ; OTHER INFORMATION: Start codon: gga, Start position: nucleotide 1.
 US-10-084-846A-3

Alignment Scores:
 Pred. No.: 0.0119 Length: 19695
 Score: 125.00 Matches: 57
 Percent Similarity: 35.29% Conservative: 15
 Best Local Similarity: 27.94% Mismatches: 68
 Query Match: 11.72% Indels: 64
 DB: 15 Gaps: 11

US-09-920-953-2 (1-598) x US-10-084-846A-3 (1-19695)
 QY 2 CGCTCCGTGCAAGC---CGGCCACACACACAGACGCGGAGCGGATCGCGGC 58
 Db 11324 ArgCysAlaGlyThrSerAlaSerProAlaSerThrArgSerArgSerProAla 11343
 QY 59 GCAACA-----AGCTGTTTGATGACCTGGCGGCGCAGAGCATGAGC 103
 Db 11344 AlaArgThrTyrArgGlyAlaAlaSerThrThrProAlaAlaGlyArgArg----- 11361
 QY 104 TGGCGGTTGACACCTTTCACGATAGG-----TCCTGG----- 136
 Db 11362 -----SerAlaValArgLysAsnCysTrpSerSerThrProArgPro 11376
 QY 137 -----CTGACCGGAGCTGCTGCCCTTTTCGAGTCCCTGACATGC 178
 Db 11377 ProThrSerGlySerSerThrThrArgAlaValCysGlyAlaGlySerThrTrpProPro 11396
 QY 179 AAGACGAGAGATGAAGCAGGTCAAGTTCA-----TGAGCTTCGTGTTG 223
 Db 11397 AspSerProCysProArgCysSerSerTrpThrSerProProAlaSerThrArg 11416
 QY 224 CGGAGCAGAC-----AATACAGGCGGAGCATGT 256

Db 11417 AlaThrAlaThrArgSerGlyArgTrpSerValArgTrpSerSerArgAlaProProCys 11436
 QY 257 AGACACACACGCCCATCTGTCAAGGCCACGGCTGGACACCGCCACTTTTGACAGA 316
 Db 11437 CysSerProArgSerThrTrpArgArg-----ProThrGlySerProThrArg 11452
 QY 317 TCAGACAGTACCTTGTGAGAGACGCTGCAAGAGATGGCGTCAAGCAGGATGTGATCCAGC 376
 Db 11453 SerArgSerThr-----ArgAlaAlaGlySerSerArgAlaProPro 11466
 QY 377 AGCCCGCCGAGTGTGGAGT-----CCACCCCGCAGC--- 409
 Db 11467 ArgProSerProTrpTrpAlaAlaThrGlySerTrpProTrpArgProProArgThrCys 11486
 QY 410 -----AATTGACTTCCCAACACTGGCAGCCCACTGATTTTCAATTAACCCAC 460
 Db 11487 ArgProProArgLysSerProAlaSerArgGlyProSerProArgTrpThrProArg 11506
 QY 461 CCAGCCTGAGC 472
 Db 11507 ProAlaValSer 11510

RESULT 6
 US-10-084-846A-6
 ; Sequence 6, Application US/10084846A
 ; Publication No. US20040006026A1
 ; GENERAL INFORMATION:
 ; APPLICANT: WEITNAUER, GABRIELE
 ; APPLICANT: MUHLENWEG, AGNES
 ; APPLICANT: TREPZER, AXEL
 ; APPLICANT: BECHTHOLD, ANDREAS
 ; TITLE OF INVENTION: AVILAMYCIN DERIVATIVES
 ; FILE REFERENCE: 1974-005
 ; CURRENT APPLICATION NUMBER: US/10/084,846A
 ; PRIOR FILING DATE: 2003-02-25
 ; PRIOR APPLICATION NUMBER: PCT/EP01/09815
 ; PRIOR FILING DATE: 2001-08-24
 ; PRIOR APPLICATION NUMBER: DE 101 09 166.4
 ; PRIOR FILING DATE: 2001-02-25
 ; NUMBER OF SEQ ID NOS: 120
 ; SOFTWARE: PatentIn Ver. 3.2
 ; SEQ ID NO 6
 ; LENGTH: 19662
 ; TYPE: PRT
 ; ORGANISM: Streptomyces viridochromogenes
 ; FEATURES:
 ; OTHER INFORMATION: Protein 1: amino acid sequence encoded by coding strand 2.
 ; OTHER INFORMATION: Start codon: gga, Start position: nucleotide 1.
 US-10-084-846A-6

Alignment Scores:
 Pred. No.: 0.0133 Length: 19662
 Score: 124.50 Matches: 56
 Percent Similarity: 33.02% Conservative: 14
 Best Local Similarity: 26.42% Mismatches: 64
 Query Match: 11.10% Indels: 78
 DB: 15 Gaps: 10

US-09-920-953-2 (1-598) x US-10-084-846A-6 (1-19662)
 QY 536 GTCCTGGCCCGCTGGCGCGCTCGCAACTGGCG---CTCCCGCTCAAAATCGATGG 480
 Db 19332 AlaProGlyArgProProArgProArgProCysAlaGlyPheProThr----- 19347
 QY 479 AATGACGCTCAGCTGGGTTGGGTTAATGAATCAGTTGGGTGGCAGTTGTTGGN 420
 Db 19348 -----ProGlyProGlyTrp----- 19352
 QY 419 AAGTCAAAATTCGTCGGGTGGACTCCACCACTCGCGGGGCTGCTGATCAGATCC--- 363
 Db 19353 -----AlaAlaAlaCysSerAlaAlaProCysSerCysSerAlaThrSerThr 19368

RESULT 7

Alignment Scores:		
Pred. No.:	0.0321	Length: 19608
Score:	120.50	Matches: 49
Percent Similarity:	35.71%	Conservative: 16
Best Local Similarity:	26.92%	Mismatches: 92
Query Match:	11.29%	Indels: 25
DB:	15	Gaps: 7

US-09-920-953-2 (1-598) x US-10-084-846A-8 (1-19608)

Alignment Scores:	
Pred. No.:	0.0149
Score:	119.50
Percent Similarity:	35.08%
Best Local Similarity:	27.23%
Mismatches:	69
Matches:	52
Length:	276

Alignment Scores:

Pred. No.:	0.0149	Length:	276
Score:	119.50	Matches:	52
Percent Similarity:	35.08%	Conservative:	15
Best Local Similarity:	27.23%	Mismatches:	69

```

Query Match: 11.20% Indels: 55
DB: 16 Gaps: 8
US-09-920-953-2 (1-598) x US-10-425-114-72136 (1-276)

QY 29 CCACAGACGGCGGAGCGGATCGCGCGCAAGAGCTGTTGATGACCTGGCGCGC 88
DB 3 ProArgArgArgArgArgArgileCysThrValArg----- 14
QY 89 CAGAGGCATGAAGCTGGCGGTGTACACCTTCTACGATAAGTGCTGGCTGACCGGAGC 148
DB 15 -----ArgProThrAlaThrThr-----ThrThrThrSer 25
QY 149 TGTGCTCTCTTCGAGTCCCTGGACATGCAAGACGAGAGATGAAGCAGGTCAAGTTCA 208
DB 26 AlaSerProSerSerSerProThrPro-----GlySerSerProGly 39
QY 209 TGAGCTTCGTGTTGGCGGAGCAGACCAATACAGGCGCGAAGCATGTACGACG----- 262
DB 40 AlaAlaSerCysAlaThrSerSerAlaAlaSerArgAlaThrArgThrSerThrAlaPro 59
QY 263 ---CACACGCCCATCTGTCAAGGCGCAGCGCTCGACACCGCCACCTTTCACAGATCA 319
DB 60 ProSerSerProSerHisGlySerArgSerProTrpThrGlyThrThrSerSerProSer 79
QY 320 AGCAGTACCTTGAGAGACGCTGC-----AGAGATGGCGCTCAAGCAGGATGTA 370
DB 80 ArgSerGlySerCysArgGlyCysPheArgArgArgTrpArgSerThrArg----- 97
QY 371 TCACAGCAGCCCGCGAGTGGTGGAGTCCACCGCGCAGCAATTGACTTNCACCAACT 430
DB 98 -----ProAlaAlaProSerSerAlaSerProThrGly 108
QY 431 GGCACCCCACTGATTTCATTAAACCAACCCAGCCCTGAGGCTCATCTCCATGATTTT 490
DB 109 AlaSerThrThrSer-----ProSerProThr----- 117
QY 491 GAGCGGGAGCGCCAGTTCGCGAGCGCGCCAGGGGGCCAGGAGCTGCAAAATCGTTTG 550
DB 118 -----ProAlaAlaArgAlaAlaSerGlyAlaProAlaAspGlySer**Cys 133
QY 551 CCAGCCCTTGTGCATTGAAGCCATCAGCCA 583
DB 134 SerGlyArgAlaProArgGluSerSerAlaPro 144

RESULT 9
US-10-425-114-72136
; Sequence 72136, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Zhou, Yihua
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 72136
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3245-558-A1_FLI.pep
US-10-425-114-72136

Alignment Scores: 0.025 Length: 384
Pred. No.: 117 50 Matches: 69
Score:

```

Percent Similarity: 37.95% Conservative: 16
Best Local Similarity: 30.80% Mismatches: 74
Query Match: 11.01% Indels: 65
DB: 12 Gaps: 13

US-09-920-953-2 (1-598) x US-10-425-114-72136 (1-384)

QY 15 CGCGCCACAGCAC-----CACAGACGGCGGAGCGGATCGCGCGCAAGAGCT 68
DB 54 ArgGlyHisArgHisSerHisArgProLeuAlaSerGlyArgGln----- 69
QY 69 GTTTGATGACCTGGCGGCGCAGAGCATGAAGCTGGC----- 107
DB 70 -----ArgArgArgArgGlyArgAlaGlyArgArgGlyGlyArgGlyGlu 84
QY 108 ---GGTGAACACTTCTACGA-----TAAGTGCT 134
DB 85 ProGlyLeuGlyLeuLeuArgGlyArgGlyProArgAlaArgAspArgGlyAla 104
QY 135 GGCTGACCGCGGCTGCTGCCCTTCTCGAGTCCCTGGACATGCA-----AGAGCA 185
DB 105 ArgAspGlyGlyAlaAlaArgValLeuArgAlaAlaGlyArgAlaGlyArgGlyAla 124
QY 186 GAAGATGAAGCAGCTCAAGTTCATGAGCTTCGTTGGCGGAGCAGACCAATACAAGG 245
DB 125 GluGluArgGlyGlyAlaAlaArgValLeuArgValGlyAlaHisGlnGluArgGly 144
QY 246 -----CCGAGCATGTACGACGACACGCGCCATCTGTCAGGGCCA 287
DB 145 LeuGluGlyGlyValArgProArgAlaAlaArgAlaAlaAlaGlySerArgGlyArg 164
QY 288 CGG-----CTGGACCAACCGCCACTTTGACAAGATCAA 320
DB 165 ArgArgAlaArgValArgGluGlnValAlaProGlySerAlaGlyLeu---GlnArgGly 183
QY 321 GCAGTACCTTGGAGACCGCTGCAAGAGATGGCGT-----CAACGAGGATGT 368
DB 184 AlaGlyGlyValArgGluSer-----AspGlyArgAlaGlyValGlnAlaGlyAla 201
QY 369 GATCCAGCAGCGCGCGGAGTGTGGAGTCCACCGCGCAGCAAT---TTGACTTCCCAA 425
DB 202 Asp--ArgProGluProGluAlaGluAlaArgProAlaAlaArgLeuGlnGlyProA 221
QY 426 CAACTCGCACCAACTGATTTTCAATTAACCAACCCAGCTGAGCGCTCATTCATCG 485
DB 221 spAspLeuHisProAlaGlu-----ProLeuProSerMetProGlu----- 234
QY 486 ATTTTGAGCGGGGCGCGCGAGTTCGCGAGCGCGCGCGCGCGCGCGCGCGCGCAATC 545
DB 235 -----ProArgProGlyProArgArgGlyThrAlaGlnGlyArgArgProAspHisP 253
QY 546 GTTTGCCA 553
DB 253 roValPro 255

RESULT 10
US-10-425-114-72137
; Sequence 72137, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 72137
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3245-558-A1_FLI.pep
US-10-425-114-72136

APPLICANT: BECHTHOLD, ANDREAS
TITLE OF INVENTION: AVILAMYCIN DERIVATIVES
FILE REFERENCE: 1974-005
CURRENT APPLICATION NUMBER: US/10/084,846A
CURRENT FILING DATE: 2003-02-25
PRIOR APPLICATION NUMBER: PCT/EP01/09815
PRIOR FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: DE 101 09 166.4
PRIOR FILING DATE: 2001-02-25
NUMBER OF SEQ ID NOS: 120
SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 5
LENGTH: 19723
TYPE: PRT
ORGANISM: Streptomyces viridochromogenes
FEATURE:
OTHER INFORMATION: Protein 3: amino acid sequence encoded by coding strand 1.
OTHER INFORMATION: Start codon: atc, Start position: nucleotide 3.
US-10-084-846A-5

Alignment Scores:
Pred. No.: 0.0624 Length: 19723
Score: 117.50 Matches: 64
Percent Similarity: 32.91% Conservative: 13
Best Local Similarity: 27.35% Mismatches: 86
Query Match: 10.47% Indels: 71
DB: 15 Gaps: 15

US-09-920-953-2 (1-598) x US-10-084-846A-5 (1-19723)

QY 556 GCCTGCGCAACGATTGTCAGGCTCTGGCGCCCTGGCGCGCTCGGC----- 509
Db 16445 GYAlaGlnArgGlyHisArgThrGlyProGlyLysSerGlyAlaGlyProGly 16464
QY 508 -----AACTGGCGCTCCCGCTCAAAATCGATGAATG 476
Db 16465 ThrAlaAlaArgGlnArgLeuValArgSerArgTrpProMetSerAlaSerAlaPhe 16484
QY 475 ACCGCTCAGCTGGGGTGGTTAATGAAATCATGTTGGTGGCGAGTTGT----- 425
Db 16485 SerTrpLeuValGlyArgGly-----SerTrpAlaValSerCysAlaArgThr 16500
QY 424 -----TGG-----GNAAGTCAAAATTCGT 407
Db 16501 ProArgProGluProArgTrpArgSerProGlyGlyTyrArgThrSerProCysArg 16520
QY 406 CGCGGG-----TGAATCCACCTCCGGCGGCTGTGATCATCATCTCTCTGTA 356
Db 16521 AlaGlySerSerSerTrpThrSerPro---ProArgArgProGlyAsnTrpProThrSer 16539
QY 355 CGCCCATCTCTGACAGCGTCTCCCAAGGTACTGCTTGTCTTGTCAAGTGGCGGTGT 296
Db 16540 ThrProSer-----AlaArgThrArgTrpSerThrProSerAlaAlaThrGlyGlySer 16557
QY 295 CCAGCGCGTGGCGCTTGACCATGGCGTGTGCGT---CGTACATGCTTCGGCCCTTGT 239
Db 16558 ProAsnGlyThrTrpArgProThrAlaArgCysArgProAlaAlaCysTrpThrArgCys 16577
QY 238 ATTGCTGTCTCCGCCAAACAGAGCTCATGAATTCACCTGCTTCTCTCTCTCTT 179
Db 16578 GlyGly-----ProArgAlaVal-----ProThrSerSerThrSerAla 16590
QY 178 GCATGT-----CCAGGGACTCGAAGAAGG--- 155
Db 16591 GlnCysTrpSerThrAlaArgProArgProValaenArgProGlyProArgArgArgPro 16610
QY 154 GCAGCAGCTCCGGGTTCAGCGACCTTATCGTAGAAGGTGTCAACCCGAGCTTCATCC 95
Db 16611 GlyArgArgProProThrAlaArgProAsnSerArgArgAlaArgPro-----Cys 16627
QY 94 CTCTGT-----CGCCGCCAGGTTCATCAACAGCTTCTCTTGG----- 59
Db 16628 TrpArgProProArgArgAlaSerTrpArgArgAlaCysGlySerProThrTrpPro 16647

LENGTH: 384
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: LIB3061-057-C6_FLI.pep
US-10-425-114-72137

Alignment Scores:
Pred. No.: 0.025 Length: 384
Score: 117.50 Matches: 69
Percent Similarity: 37.95% Conservative: 16
Best Local Similarity: 30.80% Mismatches: 74
Query Match: 11.01% Indels: 65
DB: 12 Gaps: 13

US-09-920-953-2 (1-598) x US-10-425-114-72137 (1-384)

QY 15 CGCGGCCACAGAC-----CACAGACGGCGGAGCGGATGCGGGCGCAGAGCT 69
Db 54 ArgGlyHisArgHisSerHisArgProLeuAlaSerGlyArgGln----- 69
QY 69 GTTTGATGACCTGGCGCGCGCAGAGCATGAAGCTGGC----- 107
Db 70 -----ArgArgArgArgGlyArgAlaGlyArgGlyArgGlyGlu 84
QY 108 ---GGTTGACACCTTCTACGA-----TAAGTGTCT 134
Db 85 ProGlyLeuGlyLeuLeuArgGlyArgGlyProArgArgAlaArgAspArgGlyAla 104
QY 135 GGCTGACCGGAGCTGCTTCGAGTCCCTCGACATGCA-----AGAGCA 185
Db 105 ArgAspGlyGlyAlaAlaArgValLeuArgAlaAlaGlyArgAlaGlyArgGlyAla 124
QY 186 GAAGATGAACGAGTCAAGTTTCATGCTTCGTTGGCGGAGCAGACCAATACAGGG 245
Db 125 GluGluArgGlyGlyAlaAlaArgValLeuArgValGlyAlaHisGlnGluArgGly 144
QY 246 -----CCGAGCATGTACGACGCACACGCCCATCTGTCAGGCGCA 287
Db 145 LeuGluGlyValArgProArgAlaAlaArgAlaAlaAlaAlaGlySerArgGlyArg 164
QY 288 CGG-----CCTGGACCCCGCCACTTTCACAGATCAA 320
Db 165 ArgArgAlaArgValArgGluGlnValAlaProGlySerAlaGlyLeu---GlnArgGly 183
QY 321 GCAGTACTTGGAGACGCTGCMAGAGATGGGGT-----CAAGCAGATGT 368
Db 184 AlaGlyGlyValArgGluSer-----AspGlyArgAlaGlyValGlnAlaGlyAla 201
QY 369 GATCCAGCAGCGCGCGAGTGGTGGAGTCCACCGCGACGAAT---TTGACTTCCCAA 425
Db 202 Asp---ArgProGluProGluAlaGluAlaArgProAlaAlaArgLeuLeuGlnGlyProA 221
QY 426 CAATCGCGCCCACTGATTTCATTAAACCCACCCAGCTGAGCGCTCATTCATCG 485
Db 221 spAspLeuHisProAlaGlu-----ProLeuProSerMetProGlu----- 234
QY 486 ATTTGACGGGAGCGCCAGTTCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 545
Db 235 -----ProArgProGlyProArgArgGlyThrAlaGlnGlyArgArgProAspHisP 253
QY 546 GTTTGCCA 553
Db 253 roValPro 255

RESULT 11
US-10-084-846A-5
Sequence 5, Application US/10084846A
Publication No. US20040006026A1
GENERAL INFORMATION:
APPLICANT: WEITNAUER, GABRIELE
APPLICANT: MUHLNBERG, AGNES
APPLICANT: TREFFER, AXEL

QY 58 GCCCGCATCCCGTTCGCGCTCTGTGGTGCTGGTGGCG 17
 Db 16648 GlyArgAlaProArgArgSerAlaCysSerAlaGlyTrpPro 16661

RESULT 12

US-10-084-846A-7
 ; Sequence 7, Application US/10084846A
 ; Publication No. US20040006026A1
 ; GENERAL INFORMATION:
 ; APPLICANT: WEITNAUER, GABRIELE
 ; APPLICANT: MUHLNBERG, AGNES
 ; APPLICANT: TREPZER, AXEL
 ; APPLICANT: BECHTHOLD, ANDREAS
 ; TITLE OF INVENTION: AVILAMYCIN DERIVATIVES
 ; FILE REFERENCE: 1974-005
 ; CURRENT APPLICATION NUMBER: US/10/084,846A
 ; PRIOR FILING DATE: 2003-02-25
 ; PRIOR APPLICATION NUMBER: PCT/EP01/09815
 ; PRIOR FILING DATE: 2001-08-24
 ; PRIOR APPLICATION NUMBER: DE 101 09 166.4
 ; PRIOR FILING DATE: 2001-02-25
 ; NUMBER OF SEQ ID NOS: 120
 ; SOFTWARE: PatentIn Ver. 3.2
 ; SEQ ID NO 7
 ; LENGTH: 19652
 ; TYPE: PRT
 ; ORGANISM: Streptomyces viridochromogenes
 ; FEATURE:
 ; OTHER INFORMATION: Protein 2: amino acid sequence encoded by coding strand 2.
 ; OTHER INFORMATION: Start codon: gat, Start position: nucleotide 2.

Alignment Scores:

Pred. No.: 0.0777 Length: 19652
 Score: 116.50 Matches: 73
 Percent Similarity: 32.95% Conservative: 14
 Best Local Similarity: 27.65% Mismatches: 93
 Query Match: 10.38% Indels: 84
 DB: 15 Gaps: 13

US-09-920-953-2 (1-598) x US-10-084-846A-7 (1-19652)

QY 598 GCGTGGTGGCGAAATGCTGATGCTCTCAATGACG-----AAG 557
 Db 6432 GlyTrpProThrArgTrpThrArgProGlyCysProSerProSerProArgValArg 6451
 QY 556 GCGTGGCGAAATGCTGATGCTCTCAATGACG-----AAG 557
 Db 6432 GlyTrpProThrArgTrpThrArgProGlyCysProSerProSerProArgValArg 6451
 QY 556 GCGTGGCGAAATGCTGATGCTCTCAATGACG-----AAG 557
 Db 6432 GlyTrpProThrArgTrpThrArgProGlyCysProSerProSerProArgValArg 6451
 QY 496 CGCTCAAAATCGATGGAATGAGCGCTCAGCGTGGGTGGTAAATCAAAATCAGTTGG 437
 Db 6465 Prolie-----SerProThrArgAlaGlyProMet----- 6475
 QY 436 GTGGCGAGTTGTTGGNAAGTCAATTCG----- 407
 Db 6476 -----CysTrpSerSerTrpArgProLysArgSerProThrProSerArgAla 6492
 QY 406 CGCGGGTGGACT-----CCACCACCTCCGCGCGCTGGATCA 368
 Db 6493 ProGlyTrpThrArgThrAspValProArgProGlyArgSerThrArgSerGlyPro 6512
 QY 367 CATCTGCTTACGCCCATCTCTTCAGCGTCTCTCCAGGTACTGCTGATCTTGT--- 311
 Db 6513 ArgProLeuThrSerArgSerLeuArgProAlaAlaCysGlyThrAlaProHisThrVal 6532
 QY 310 ---CAAAGTGGGGTGGTCCAGCGCGCTTACCGAGTGGCGGTGGTGGTGGTGGTGGT 254
 Db 6533 ArgArgSerSerHisGlyProThrThrGlyProProHisAlaGlyProArgArgMetPro 6552
 QY 253 TGCCTTGGCGCTTGTATTGGTGTCTCCGCCCAACACGAACTCATGAATTTGACCT--- 197

Db 6553 AlaAlaLeuProGlySerGlyValIleuArgAlaAaArgSerArgCysArgIleProArg 6572
 QY 196 -----GCTTCATCTTCTGCTTGTGATGTCAGGACCTCGAAGA--- 158
 Db 6573 LeuArgArgProArgAlaArgSerArgProGlySerArgCysProCysProArgArgGlu 6592
 QY 157 ---AGGCGACAGCTCCGCGTCCAGCCAGCA-----CCTTATCGTAGAAGGTGTCAACG 107
 Db 6593 CysArgSerArgArgProArgArgProSerHisProAlaArgThrArgCysArgPro 6612
 QY 106 CCAGCT-----TCATGC 95
 Db 6613 ThrAlaArgProGlyThrTrpProAlaProArgValArgArgAlaGlyArgAla 6632
 QY 94 CTTCTGCGCGCGCGAGTCAACACAGCT----- 65
 Db 6633 AlaAlaArgArgProHisArgSerAlaArgSerArgThrGlyCysArg 6652
 QY 64 ---TCTTGGCGCGCGATCCCGTTCGCGCTCTCTGT---GGTGTGGTGGCGCGCTCTG 11
 Db 6653 ArgSer-ThrProAlaProArgAlaArgProAlaProGlyAlaGlyArgArgAl 6672
 QY 10 CAGGCGAGCGC 1
 Db 6672 aargThrArg 6675

RESULT 13

US-10-437-963-103601
 ; Sequence 103601, Application US/10437963
 ; Publication No. US20040123343A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Wu, Wei
 ; APPLICANT: Boukharov, Andrey A.
 ; APPLICANT: Barbazuk, Brad
 ; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
 ; FILE REFERENCE: 38-21(53221)B
 ; CURRENT APPLICATION NUMBER: US/10/437,963
 ; CURRENT FILING DATE: 2003-05-14
 ; NUMBER OF SEQ ID NOS: 204966
 ; SEQ ID NO 103601
 ; LENGTH: 155
 ; TYPE: PRT
 ; ORGANISM: Oryza sativa
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT4530_101013C.1.pep
 ; US-10-437-963-103601

Alignment Scores:

Pred. No.: 0.0315 Length: 155
 Score: 115.50 Matches: 48
 Percent Similarity: 36.91% Conservative: 7
 Best Local Similarity: 32.21% Mismatches: 43
 Query Match: 10.29% Indels: 45
 DB: 16 Gaps: 9

US-09-920-953-2 (1-598) x US-10-437-963-103601 (1-155)

QY 385 CGCGCGCGTGGATCATCATCTCTTTCAGCGCTCTTTCAGCGTCTTTCAGGT 326
 Db 19 ArgArgArgAlaProThrHisGluPro-----ProSerSerProArgAlaGlyArgSer 36
 QY 325 ACTGCTTGATCTTGTCAAGTGGCGGT-----GGTCCAGCGCGTGGC 284
 Db 37 ArgSerArgSerCysThrSerAlaProArgArgCysHisArgIleAlaProGlyArgGly 56
 QY 283 -----CCTTACAGAGTGGCGCTGTCGCTGATACATGC 251


```
QY 54 CGGGCCCAAGAGCTGTTTGTATGACCTGGGGGGGAGAGGAGCATGAGCTGGCGGTGA 113
Db 109 HisAlaaspArgGlyGlnHisValProGlyArgAlaArgGluArgArgGlyGln 128
QY 114 CACCTT-----CTAGATAAGGTGCTGCTCACCGGAGCTGCTGCCCTTCTTGA 164
Db 129 HisCysHisAlaHisHisArgGluaspAlaAlaTrpProGlyAlaArgValLeu----- 146
QY 165 GTCCCTGGACATGCA-----AGAGCA 185
Db 147 GlyProGlyHisAlaGlyValProArgArgaspValAlaAlaValAlaArgVal 166
QY 186 GAAGATGAAGCAGGTCAAGTTCATGACTTCGTGTTTGGCGGAGCAGACCAATACAGGG 245
Db 167 HisLeuArgLeuProAlaValHisGlnArgArgValProHisArgGlnProaspGln--- 185
QY 246 CCGAAGCATGTACGAGC-----ACACGCCCATCTGCT--- 278
Db 186 LeuArgHisValAlaaspProArgValGlyMetAlaProValAlaArgProArgGlyVal 205
QY 279 -----CAAGGCCACGGCTGGACCCGCCACTTGTGACAAGATCAAGCAGTA 326
Db 206 ProGlyArgArgHisGlyGlyArgGlyValHisProGlyHisAlaGluGlnProGly 225
QY 327 CCTTGGAGAGACGCT-----GCAAGAGATGGCGT 356
Db 226 ProAlaArgGluAlaArgProArgProArgAlaProAlaGlyAlaArgGlnGlyArg 245
QY 357 CAAGCAGGATGTATCCAGCAGCGCCGAGTGTGTGAGTCCACCCGCGACGAATTGA 416
Db 246 Arg-----ArgArgArgValGlnArgHisProArgArgArgGly 259
QY 417 CTTNCCCAACTGGCCACCACTGATTTTCATTAACCCAAACCCAGCCTGAGCGCTC 476
Db 260 AlaArgProGlnGluArgArgGlyArgValProAlaaspProAla-----AlaArg 276
QY 477 ATTCCATCGAATTTGAGCGGGAGCGCCAGTTGCGAGCGCGCCGAGGGGCCOAGG 533
Db 277 ValProAlaValProGlyHisGlyHisArgValProGlyValProGlnProHisArg 295
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Search completed: July 19, 2004, 17:30:09
Job time : 96 secs